	Hits	Search Text	DBs	Time Stamp
1	4	(("6140087") or ("6379943")).PN.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/07 08:41
2	2	("6140087").PN.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/07 08:41
3	1	"5882877".PN.	USPAT	2002/08/01 08:51
4	2	("6379943").PN.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/08/01 14:34
5	0	head-to-head adj ITR	USPAT	2002/08/01 14:40
6	2	ITR adj1 junction	USPAT	2002/08/01 14:40

left inverted terminal repeat, or ITR, (bp 1 to approximately 103) the packaging signals (approximately 194 to 358 bp) (Hearing and Shenk, 1983, Cell 33: 695-703; Grable and Hearing 1992, J. Virol. 64: 2047-2056) and the right ITR.

contains ITR junctions which are known to be fuctionally capable of generating replicating linear Ad DNA molecules (Graham, F.L., "Covalently closed circles of human adenovirus DNA are infections," The EMBO J. 3, 2917-2922, 1984).

L9 ANSWER 1 OF 2 MEDLINE
ACCESSION NUMBER: 97284920 MEDLINE
DOCUMENT NUMBER: 97284920 PubMed ID: 9140193
TITLE: Structural and functional heterogeneity of integrated recombinant AAV genomes.
AUTHOR: Duan D; Fisher K J; Burda J F; Engelhardt J F
CORPORATE SOURCE: Wistar Institute, Philadelphia, Pennsylvania, USA.
CONTRACT NUMBER: RO1 DK/HL51887 (NIDDK)
SOURCE: VIRUS RESEARCH, (1997 Apr) 48 (1) 41-56.
Journal code: 8410979. ISSN: 0168-1702.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199707
ENTRY DATE: Entered STN: 19970812
Last Updated on STN: 19970812
Entered Medline: 19970731

AB Adeno-associated Virus (AAV) has emerged as a promising vector for gene therapy because of its ability to generate high titer recombinant stocks and the potential for site specific integration. However, much of the current knowledge regarding the transduction and integration biology of this virus is based on studies evaluating wild type AAV or recombinant AAV which was unknowingly contaminated with wild type virus. Given the fact that recombinant AAV is replication incompetent, by virtue of deleted viral rep proteins responsible for site specific integration of the wild type virus, the integration process for recombinant AAV may likely be different from its wild type counterpart. To this end, the present study has attempted to elucidate the proviral structure of stably integrated recombinant AAV genomes harboring the alkaline phosphatase reporter gene in 293 and IB3 cell lines. Initial studies attempted to functionally characterize differences in proviral genomes using mobilization assays with assessed both liberated episomal recombinant AAV and infectious virus following transfection with Rep/Cap containing plasmids and/or infection with recombinant **adenovirus** (Ad). Using Southern and polymerase chain reaction (PCR) analysis, evaluation of genomic DNA from AAV clonal cell lines indicated that head to tail orientations of **ITRs** were absolutely required for excision of episomal genomes and rescue of infectious recombinant virus. Furthermore, mobilization of proviral DNA could be achieved in the presence of exogenous Rep/Cap without **adenovirus**, while mobilization of infectious recombinant virus required the addition of both Rep/Cap and Ad. Genomic Southerns suggest that two predominant proviral structures exist for recombinant AAV including **head** to **head** and tail to head duplex genomes. A third class of monomer proviral genomes with head to tail oriented **ITRs** was also observed. No evidence for tail to tail **ITR** oriented proviral genomes was detected in any of the clonal cell lines. Such findings have begun to lay the foundation for a clearer understanding of the mechanism of recombinant AAV integration and how this process differs from wild type AAV.

L9 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:628292 CAPLUS
DOCUMENT NUMBER: 133:233574
TITLE: Enhanced system for construction of **adenovirus** vectors

INVENTOR(S): Graham, Frank L.; Parks, Robin; Ng, Philip
PATENT ASSIGNEE(S): Merck & Co., Inc., USA
SOURCE: PCT Int. Appl., 161 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000052187	A2	20000908	WO 2000-US5844	20000303
WO 2000052187	A3	20001221		
WO 2000052187	C2	20020711		
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6379943	B1	20020430	US 1999-263650	19990305
EP 1159439	A2	20011205	EP 2000-912186	20000303
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.:
US 1999-263650 A 19990305
US 1999-415899 A 19991008
WO 2000-US5844 W 20000303

AB In the present invention, viruses, plasmids or both are constructed which contain viral DNA, either at least one **head**-to-**head** **ITR** junction, recombinase recognition sites positioned such that site-specific recombination between recombinase recognition sites in sep. plasmids results in generation of infectious viral DNA at high-efficiency in cotransfected host cells that have been engineered to express a site-specific recombinase, or both. Because of the high-efficiency and specificity of the Cre enzyme, the FLP enzyme, or both, suitably engineered plasmids can be readily recombined to produce infectious virus at high-efficiency in cotransfected 293 cells, without, at the same time, producing wild-type **adenovirus**, with the attendant problems for removal thereof. Use of recombinases besides Cre or FLP, and recombinase recognition sites besides lox or frt sites, and use of cells other than 293 cells are also disclosed and enabled, as are kits incorporating the site-specific vector system, as well as compns. and methods for using such compns. as vaccines or in gene therapeutic applications. Enhancements in the efficiency of both site-specific and homologous recombination are provided by inclusion of at least one **head**-to-**head** **ITR** junction.

L11 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:628292 CAPLUS
DOCUMENT NUMBER: 133:233574
TITLE: Enhanced system for construction of **adenovirus** vectors
INVENTOR(S): Graham, Frank L.; Parks, Robin; Ng, Philip
PATENT ASSIGNEE(S): Merck & Co., Inc., USA
SOURCE: PCT Int. Appl., 161 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000052187	A2	20000908	WO 2000-US5844	20000303
WO 2000052187	A3	20001221		
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W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6379943	B1	20020430	US 1999-263650	19990305
EP 1159439	A2	20011205	EP 2000-912186	20000303
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1999-263650 A 19990305
US 1999-415899 A 19991008
WO 2000-US5844 W 20000303

AB In the present invention, viruses, plasmids or both are constructed which contain viral DNA, either at least one **head**-to-**head** ITR junction, recombinase recognition sites positioned such that site-specific recombination between recombinase recognition sites in sep. plasmids results in generation of infectious viral DNA at high-efficiency in cotransfected host cells that have been engineered to express a site-specific recombinase, or both. Because of the high-efficiency and specificity of the Cre enzyme, the FLP enzyme, or both, suitably engineered plasmids can be readily recombined to produce infectious virus at high-efficiency in cotransfected 293 cells, without, at the same time, producing wild-type **adenovirus**, with the attendant problems for removal thereof. Use of recombinases besides Cre or FLP, and recombinase recognition sites besides lox or frt sites, and use of cells other than 293 cells are also disclosed and enabled, as are kits incorporating the site-specific vector system, as well as compns. and methods for using such compns. as vaccines or in gene therapeutic applications. Enhancements in the efficiency of both site-specific and homologous recombination are provided by inclusion of at least one **head**-to-**head** ITR junction.

L11 ANSWER 2 OF 11 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 1
ACCESSION NUMBER: 2000:226342 CAPLUS
DOCUMENT NUMBER: 133:130464
TITLE: An enhanced system for construction of adenoviral vectors by the two-plasmid rescue method
AUTHOR(S): Ng, P.; Parks, R. J.; Cummings, D. T.; Evelegh, C. M.; Graham, F. L.

CORPORATE SOURCE: Department of Biology, McMaster University, Hamilton, ON, L8S 4K1, Can.
SOURCE: Human Gene Therapy (2000), 11(5), 693-699
CODEN: HGTHE3; ISSN: 1043-0342
PUBLISHER: Mary Ann Liebert, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The two-plasmid rescue method of constructing Ad vectors, which relies on either homologous or Cre-mediated recombination between two plasmids cotransfected into 293 or 293Cre4 cells, resp., offers advantages over other approaches because of its simplicity. We have improved the efficiency of vector construction by both homologous and Cre-mediated recombination by replacing the single ITR in the shuttle plasmid with a **head**-to-**head** ITR junction. We have also expanded the versatility of this method by incorporating a Cre expression cassette into the plasmids to permit high-efficiency Cre-mediated vector rescue using 293 cells, abrogating the need for Cre-expressing cell lines. This new system retains the simplicity of the original but results in an .apprx.100-fold increase in the no. of recombinant viruses produced, all of which contain the foreign DNA insert, and allows high-efficiency Cre-mediated vector isolation using any E1-complementing cell line.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 11 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 97284920 MEDLINE
DOCUMENT NUMBER: 97284920 PubMed ID: 9140193
TITLE: Structural and functional heterogeneity of integrated recombinant AAV genomes.
AUTHOR: Duan D; Fisher K J; Burda J F; Engelhardt J F
CORPORATE SOURCE: Wistar Institute, Philadelphia, Pennsylvania, USA.
CONTRACT NUMBER: RO1 DK/HL51887 (NIDDK)
SOURCE: VIRUS RESEARCH, (1997 Apr) 48 (1) 41-56.
Journal code: 8410979. ISSN: 0168-1702.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199707
ENTRY DATE: Entered STN: 19970812
Last Updated on STN: 19970812
Entered Medline: 19970731

AB Adeno-associated Virus (AAV) has emerged as a promising vector for gene therapy because of its ability to generate high titer recombinant stocks and the potential for site specific integration. However, much of the current knowledge regarding the transduction and integration biology of this virus is based on studies evaluating wild type AAV or recombinant AAV which was unknowingly contaminated with wild type virus. Given the fact that recombinant AAV is replication incompetent, by virtue of deleted viral rep proteins responsible for site specific integration of the wild type virus, the integration process for recombinant AAV may likely be different from its wild type counterpart. To this end, the present study has attempted to elucidate the proviral structure of stably integrated recombinant AAV genomes harboring the alkaline phosphatase reporter gene in 293 and IB3 cell lines. Initial studies attempted to functionally characterize differences in proviral genomes using mobilization assays with assessed both liberated episomal recombinant AAV and infectious virus following transfection with Rep/Cap containing plasmids and/or infection with recombinant **adenovirus** (Ad). Using Southern and polymerase chain reaction (PCR) analysis, evaluation of genomic DNA from AAV clonal

cell lines indicated that head to tail orientations of ITRs were absolutely required for excision of episomal genomes and rescue of infectious recombinant virus. Furthermore, mobilization of proviral DNA could be achieved in the presence of exogenous Rep/Cap without **adenovirus**, while mobilization of infectious recombinant virus required the addition of both Rep/Cap and Ad. Genomic Southerns suggest that two predominant proviral structures exist for recombinant AAV including **head** to **head** and tail to head duplex genomes. A third class of monomer proviral genomes with head to tail oriented ITRs was also observed. No evidence for tail to tail ITR oriented proviral genomes was detected in any of the clonal cell lines. Such findings have begun to lay the foundation for a clearer understanding of the mechanism of recombinant AAV integration and how this process differs from wild type AAV.

L11 ANSWER 4 OF 11 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 94088512 MEDLINE
DOCUMENT NUMBER: 94088512 PubMed ID: 8264583
TITLE: Nonhomologous recombination in human cells.
AUTHOR: Derbyshire M K; Epstein L H; Young C S; Munz P L; Fishel R
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics, University of Vermont School of Medicine, Burlington 05405.
CONTRACT NUMBER: CA-56542 (NCI)
GM-31452 (NIGMS)
NCI NO1-CO-74101 (NCI)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, (1994 Jan) 14 (1) 156-69.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199401
ENTRY DATE: Entered STN: 19940209
Last Updated on STN: 19980206
Entered Medline: 19940121

AB Nonhomologous recombination (NHR) is a major pathway for the repair of chromosomal double-strand breaks in the DNA of somatic cells. In this study, a comparison was made between the nonhomologous end joining of transfected **adenovirus** DNA fragments in vivo and the ability of purified human proteins to catalyze nonhomologous end joining in vitro. **Adenovirus** DNA fragments were shown to be efficiently joined in human cells regardless of the structure of the ends. Sequence analysis of these junctions revealed that the two participating ends frequently lost nucleotides from the 3' strands at the site of the joint. To examine the biochemical basis of the end joining, nuclear extracts were prepared from a wide variety of mammalian cell lines and tested for their ability to join test plasmid substrates. Efficient ligation of the linear substrate DNA was observed, the in vitro products being similar to the in vivo products with respect to the loss of 3' nucleotides at the junction. Substantial purification of the end-joining activity was carried out with the human immature T-cell-line HPB-ALL. The protein preparation was found to join all types of linear DNA substrates containing heterologous ends with closely equivalent efficiencies. The in vitro system for end joining does not appear to contain any of the three known DNA ligases, on the basis of a number of criteria, and has been termed the NHR ligase. The enriched activity resides in a high-molecular-weight recombination complex that appears to include and require the human homologous pairing protein HPP-1 as well as the NHR ligase. Characterization of the product molecules of the NHR ligase reaction suggests that they are linear oligomers of the monomer substrate joined nonrandomly **head**-to-**head**

and/or tail-to-ta[redacted]. The joined ends of the products were found to be modified by a 3' [redacted]onuclease prior to ligation, a[redacted]no circular DNA molecules were detected. These types of products are similar to those required for the breakage-fusion-bridge cycle, a major NHR pathway for chromosome double-strand break repair.

L11 ANSWER 5 OF 11 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 94105122 MEDLINE
DOCUMENT NUMBER: 94105122 PubMed ID: 8278357
TITLE: Deletion of the E4 region of the genome produces **adenovirus** DNA concatemers.
AUTHOR: Weiden M D; Ginsberg H S
CORPORATE SOURCE: Department of Medicine, College of Physicians and Surgeons,
Columbia University, New York, NY 10032.
CONTRACT NUMBER: AI12052 (NIAID)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1994 Jan 4) 91 (1) 153-7.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199402
ENTRY DATE: Entered STN: 19940218
Last Updated on STN: 19940218
Entered Medline: 19940204

AB Two mutants containing large deletions in the E4 region of the **adenovirus** genome H5dl366 (91.9-98.3 map units) and H2dl808 (93.0-97.1 map units) were used to investigate the role of E4 genes in **adenovirus** DNA synthesis. Infection of KB human epidermoid carcinoma cells with either mutant resulted in production of large concatemers of viral DNA. Only monomer viral genome forms were produced, however, when mutants infected W162 cells, a monkey kidney cell line transformed with and expressing the E4 genes. Diffusible E4 gene products, therefore, complement the E4 mutant phenotype. The viral DNA concatemers produced in dl366- and dl808-infected KB cells did not have any specific orientation of monomer joining: the junctions consisted of **head**-to-**head**, **head**-to-tail, and tail-to-tail joints. The junctions were covalently linked molecules, but molecules were not precisely joined, and restriction enzyme maps revealed a heterogeneous size distribution of junction fragments. A series of mutants that disrupted single E4 open reading frames (ORFs) was also studied: none showed phenotypes similar to that of dl366 or dl808. Mutants containing defects in both ORF3 and ORF6, however, manifested the concatemer phenotype, indicating redundancy in genes preventing concatemer formation.
These data suggest that the E4 ORFs 3 and 6 express functions critical for regulation of viral DNA replication and that concatemer intermediates may exist during **adenovirus** DNA synthesis.

L11 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
ACCESSION NUMBER: 1989:19263 CAPLUS
DOCUMENT NUMBER: 110:19263
TITLE: Structures of integrated DNA containing human **adenovirus** E1A gene in transgenic mice
AUTHOR(S): Ninomiya, Takashi; Hoshi, Masaki; Yuki, Atsushi
CORPORATE SOURCE: Res. Inst. Life Sci., Snow Brand Milk Prod. Co., Ltd.,
Tochigi, 329-05, Japan
SOURCE: Agric. Biol. Chem. (1988), 52(10), 2537-46
CODEN: ABCHA6; ISSN: 0002-1369
DOCUMENT TYPE: Journal

LANGUAGE: English

AB One of the DNAs, [redacted]aron 10-gE1A-2, pSV2-gpt-gE1A, [redacted] Ad12 E1A, was microinjected sep. into pronuclei of fertilized mouse eggs, and 14 transgenic mouse lines were obtained. The structures of integrated DNAs in these transgenic mice were analyzed by Southern blot hybridization. **Head**-to-**head** and tail-to-tail structures were found, although the injected mols. had a tendency to join each other in head-to-tail tandem forms when multiple copies were integrated. The analyses of the mice contg. pSV2-gpt-gE1A showed that most of the restriction sites at the end of the injected mols. were restored at the tandem junctions. Furthermore, the integrated DNAs at the junctions to the host chromosomal DNA were deleted and (or) rearranged.

L11 ANSWER 7 OF 11 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 86144079 MEDLINE
DOCUMENT NUMBER: 86144079 PubMed ID: 2936901
TITLE: The long terminal repeat of the intracisternal A particle as a target for transactivation by oncogene products.
AUTHOR: Luria S; Horowitz M
SOURCE: JOURNAL OF VIROLOGY, (1986 Mar) 57 (3) 998-1003.
Journal code: 0113724. ISSN: 0022-538X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198603
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19980206
Entered Medline: 19860328

AB It has been shown recently that the c-mos oncogene becomes activated in myeloma XRPC-24 via insertion of an intracisternal A particle (IAP) long terminal repeat (LTR). The inserted LTR serves as a promoter from which transcription of the 3' rearranged c-mos initiates. The insertion is in a **head**-to-**head** orientation such that the transcriptional orientations of the IAP and the 3' rearranged c-mos are opposite. It has already been shown that this IAP LTR has two promoters, one transcribing the IAP genome and the other transcribing the rearranged c-mos. Since the IAP genomes are actively transcribed in mouse myelomas but not in normal cells, it was interesting to test whether transcriptional activation of the IAP occurs in the presence of active oncogene products, especially nuclear ones. The 5' LTR of the IAP inserted in myeloma XRPC-24 was chosen as a convenient model to test the effect of viral and cellular oncogene products. These included simian virus 40 (SV40) large-T antigen, the **adenovirus** early 1A (E1A) gene product, the myc gene product, and p53. The LTR was coupled to the bacterial gene coding for chloramphenicol acetyltransferase (CAT) in two orientations, and the levels of CAT directed by the LTR promoters were assayed in either the presence or the absence of the oncogene products. The levels of CAT directed by the 5' LTR promoter transcribing the IAP were significantly elevated in the presence of SV40 large-T antigen, the **adenovirus** E1A and myc gene products, and p53. The promoter transcribing the rearranged c-mos was transactivated by SV40 large-T antigen and the **adenovirus** E1A gene product. The results indicate that oncogene products may have an important role in turning on promoters of other genes. The IAP LTR may serve as a useful model for studying the effect of various gene products on promoters which are known to be activated in the malignant state.

L11 ANSWER 8 OF 11 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 86067223 MEDLINE
DOCUMENT NUMBER: 86067223 PubMed ID: 2999714
TITLE: DNA sequence of the region in the genome of herpes simplex virus type 1 containing the genes for DNA polymerase and the major DNA binding protein.

AUTHOR: Qu[redacted] J P; McGeoch D J
SOURCE: NU[redacted]IC ACIDS RESEARCH, (1985 Nov 2[redacted]13 (22) 8143-63.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M12356
ENTRY MONTH: 198601
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 19980206
Entered Medline: 19860116

AB In the long unique region of the genome of herpes simplex virus type 1 (HSV-1), the genes for DNA polymerase and the major DNA binding protein are arranged in a **head** to **head** manner, with an origin of DNA replication (termed OriL) located between them. This paper reports an 8400 base pair DNA sequence containing both genes and the origin, obtained mostly by M13/dideoxy analysis of plasmid cloned fragments. Amino acid sequences of the two proteins were deduced. Homologues of both genes were detected in the genome sequence of the distantly related Epstein-Barr virus (EBV). Arrangement of these HSV-1 and EBV genes differs in genome location and in relative orientation. A part of HSV-1 DNA polymerase was found to be similar to a sequence in **adenovirus** 2 DNA polymerase, but the significance of this is unclear. Since a DNA sequence in the locality of OriL deletes on plasmid cloning, this region was analysed using virus DNA. A palindrome with 72-residue arms was found, which shows great similarity to the better characterized origin, OriS.

L11 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 8
ACCESSION NUMBER: 1985:143990 CAPLUS
DOCUMENT NUMBER: 102:143990
TITLE: Structure and expression of the integrated viral DNA in a rat cell line transformed by the HindIII-I.cntdot.J fragment of human **adenovirus** type 7 DNA
AUTHOR(S): Yoshida, Kouichi
CORPORATE SOURCE: Cancer Res. Inst., Sapporo Med. Coll., Sapporo, Japan
SOURCE: Sapporo Igaku Zasshi (1985), 54(1), 95-105
CODEN: SIZSAR; ISSN: 0036-472X
DOCUMENT TYPE: Journal
LANGUAGE: Japanese

AB Integrated viral DNA sequences and cDNA copies of viral mRNA species were cloned from 7IJY1-1, a rat 3Y1 cell line transformed by the **adenovirus** 7 DNA fragment (HindIII-I.J 0 to 7.8% map units). The mol. arrangement and expression of the integrated HindIII-I.J fragment were analyzed. The 7IJY1-1 cell line contained most of the sequences of HindIII-I.J, which were localized at the 2 EcoRI-cleaved fragments of the cell DNA. The arrangement of viral sequences in the cell DNA was complicated, exhibiting linkages among different pieces of the HindIII-I.J in the head-to-tail or the **head**-to-**head** orientations. In 1 clone, the E1B gene region sequence was fused to the E1A gene region sequence, the structure of which was found to serve as a template for transcription of the E1B-E1A fusion mRNA of 2.0 kilobases. The cDNAs cloned were complementary to the E1B-E1A fusion mRNA of 1.8 kilobases. Sequence anal. of the cloned DNA indicated that transcription of these mRNAs initiated at or near the E1B promoter, proceeded through the E1B sequences to the flanking E1A region sequences, and terminated in the same manner as the E1A mRNAs. In vitro translation of hybridization-selected viral mRNAs showed that E1B-E1A fusion mRNAs predominantly directed the synthesis of the E1B gene-encoded protein with a mol. wt. of 16,000 (E1B-16K) and the E1A gene-encoded protein of 45,000 (E1A-45K).

L11 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 9
ACCESSION NUMBER: 1986:473465 CAPLUS
DOCUMENT NUMBER: 105:73465
TITLE: Structure and expression of the integrated viral DNA in a rat cell line transformed by the left-terminal 7.8% fragment of **adenovirus** type 7 DNA
AUTHOR(S): Yoshida, Koichi; Yaegashi, Tazuko; Kudo, Shinichi; Fujinaga, Kei
CORPORATE SOURCE: Cancer Res. Inst., Sapporo Med. Coll., Sapporo, 060, Japan
SOURCE: Tumor Res. (1985), 20, 43-60
CODEN: TUREA6; ISSN: 0041-4093
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Integrated viral DNA sequences and cDNA copies of viral mRNAs were cloned from 7IJY1-1, a rat 3Y1 cell line transformed by the **adenovirus** 7 DNA fragment (HindIII-I.cntdot.J, 0-7.8% map position). The 7IJY1-1 cell line contained most of the sequences of the HindIII-I.cntdot.J, and its mol. arrangement in the rat cell DNA was complicated, exhibiting linkages among different pieces of the HindIII-I.cntdot.J in a head to tail or a **head** to **head** orientation. Anal. of the cloned cDNA indicated that some of the fused viral DNAs serve as transcription templates for E1B-E1A fusion mRNAs which were found esp. in 7IJY1-1 cells. In vitro translation of hybridization-selected viral mRNAs showed that E1B-E1A fusion mRNAs direct the synthesis of the E1B gene-encoded 21,000-dalton protein. These results show that in the 7IJY1-1 cell line, linkage structure of the integrated HindIII-I.cntdot.J permit transcription of E1B-E1A fusion mRNAs and expression of the E1B gene-encoded 21,000-dalton protein.

L11 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1985:90645 CAPLUS
DOCUMENT NUMBER: 102:90645
TITLE: Activation of the **adenovirus** late promoter by cis- and trans-acting elements
AUTHOR(S): Lewis, E. Diann; Fu, Xin Yuan; Manley, James L.
CORPORATE SOURCE: Dep. Biol. Sci., Columbia Univ., New York, NY, 10027, USA
SOURCE: UCLA Symp. Mol. Cell. Biol., New Ser. (1984), 19(Mol. Biol. Dev.), 351-60
CODEN: USMBD6; ISSN: 0735-9543
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To study transcription initiation from a strong promoter, the **adenovirus** 2 late promoter was fused to the SV40 virus T-antigen gene A, and T-antigen protein and mRNA prodn. was examd. following transfection of the recombinant DNA into human cell lines. The promoter was activated either by a trans-acting E1A protein or by a cis-acting enhancer element. The presence of 2 enhancer elements duplicated **head**-to-**head** relative to each other gave .gtoreq.1-fold increase in transcription relative to a construct contg. only 1 copy of the enhancer element. The enhancer element had no effect on transcription in cells constitutively expressing the E1A gene.

(FILE 'HOME' ENTERED AT 08:32:12 ON 07 AUG 2002)

FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH' ENTERED AT 08:32:52 ON 07 AUG 2002

L1	80730	S	ADENOVIRUS
L2	1405	S	ITR
L3	14	S	HEAD-TO-HEAD JUNCTION
L4	0	S	L2 AND L3
L5	7434	S	HEAD-TO-HEAD OR HEAD TO HEAD
L6	21	S	L5 AND L2
L7	6	DUP	REMOVE L6 (15 DUPLICATES REMOVED)
L8	2	S	L7 AND L1
L9	2	S	L8
L10	27	S	L5 AND L1
L11	11	DUP	REMOVE L10 (16 DUPLICATES REMOVED)

	Hits	Search Text	DBs
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2	2	("6140087").PN.	USPAT; US-PGPUB; EPO; JPO; DERWENT
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4	2	("6379943").PN.	USPAT; US-PGPUB; EPO; JPO; DERWENT
5	0	head-to-head adj ITR	USPAT
6	2	ITR adj1 junction	USPAT
7	7	ITR adj1 junction	USPAT; US-PGPUB; EPO; JPO; DERWENT

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1	2002/08/07 08:41
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5	2002/08/01 14:40
6	2003/05/28 11:45
7	2003/05/28 11:45